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March 7, 2000

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## **EXPRESS MAIL LABEL NO. EL096151248US**

Box PATENT APPLICATION  
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Dear Sir:

Transmitted herewith for filing is the patent application of:

**Inventor(s): ERIC HENDERSON and MICHAEL P. LYNCH**

**For: A METHOD FOR SOLID STATE GENOME ANALYSIS**

**Our File No. 454357-5**

Enclosed are the following papers:

- (X) Specification with attached Declaration
- ( ) Specification without attached Declaration
- ( ) Formal drawings
- (X) Informal drawings (3 sets)
- ( ) Prior Art Statement under 37 C.F.R. §1.97
- ( ) Preliminary Amendment

# DORSEY & WHITNEY LLP

Assistant Commissioner for Patents

March 7, 2000

Page 2

- ( ) An Assignment of the invention in favor of the following organization is enclosed for recordation:

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Any notice that is to be furnished to the above organization after grant of the patent should be addressed to the firm of the undersigned. Any notice for any other reason should be addressed to the organization with the notation, "Attention: Office of the President".

- ( ) Payment enclosed herewith includes a \$40.00 assignment recordation fee.

- (X) Priority is hereby claimed based upon prior Provisional Application Serial No. 60/123,362 filed March 8, 1999.

- (X) The total amount due for the filing fee in this case is:

Basic filing fee, \$690 (\$345, small entity)	\$ 345.00
Independent Claims in excess of 3, \$78.00 each (\$39, small entity)	\$
Total Claims in excess of 20, \$18.00 each (\$9, small entity)	\$ 99.00
Multiple dependent claims, \$260.00 each (\$130, small entity)	\$
Assignment, \$40	\$

**GRAND TOTAL DUE** **\$ 444.00**

- (X) Where a 50% fee reduction is indicated in the calculation in the preceding paragraph, documentation making this claim under 37 C.F.R. §1.9(f) is attached.
- (X) Our payment is included in the amount of the GRAND TOTAL DUE in the following manner:
- (X) Our check in the full amount is included.
- (X) The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Account No. 04-1420.

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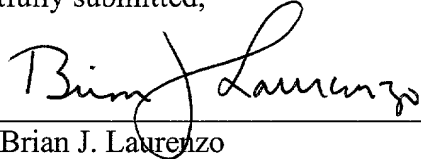
March 7, 2000

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- (X) General Authorization. This paper constitutes a general authorization to the Commissioner for all fee requirements subsequent to the instant filing to charge all fees for amendments, petitions, and any and all other papers, to our Deposit Account No. 04-1420. This is not, however, an automatic authorization to mail a Notice of Allowance with a charge of the Issue Fee.

Respectfully submitted,

By: \_\_\_\_\_

  
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Applicants: ERIC HENDERSON and MICHAEL P. LYNCH  
Serial No.: To Be Assigned  
Filed: March 7, 2000  
For: A METHOD FOR SOLID STATE GENOME ANALYSIS

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY  
STATUS (37 CFR 1.9(f) and 1.27(b)) - INDEPENDENT INVENTOR**

As a below named inventor, I hereby declare that I qualify as an independent inventor as defined in 37 CFR 1.9(c) for purposes of paying reduced fees under Sections 41(a) and (b) of Title 35, United States Code, to the Patent and Trademark Office with regard to the invention entitled A METHOD FOR SOLID STATE GENOME ANALYSIS described in

- (X) the specification filed herewith  
( ) application serial no. \_\_\_\_\_, filed \_\_\_\_\_  
( ) patent no. \_\_\_\_\_, issued \_\_\_\_\_

I have not assigned, granted, conveyed or licensed and am under no obligation under contract or law to assign, grant, convey or license, any rights in the invention to any person who could not be classified as an independent inventor under 37 CFR 1.9(c) if that person had made the invention, or to any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

Each person, concern or organization to which I have assigned, granted, conveyed, or licensed or am under an obligation under contract or law to assign, grant, convey, or license any rights in the invention is listed below:

- ( ) no such person, concern or organization  
(X) persons, concerns or organizations listed below\*

\*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

FULL NAME BioForce Laboratory, Inc.  
ADDRESS 2901 South Loop Drive, Ames, Iowa 50010  
( ) INDIVIDUAL (X) SMALL BUSINESS CONCERN ( ) NONPROFIT ORGANIZATION

FULL NAME \_\_\_\_\_  
ADDRESS \_\_\_\_\_  
( ) INDIVIDUAL ( ) SMALL BUSINESS CONCERN ( ) NONPROFIT ORGANIZATION

FULL NAME \_\_\_\_\_  
ADDRESS \_\_\_\_\_  
( ) INDIVIDUAL ( ) SMALL BUSINESS CONCERN ( ) NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

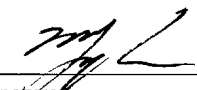
I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

ERIC HENDERSON  
Name of Inventor

  
Signature

March 2 2000  
Date

MICHAEL P. LYNCH  
Name of Inventor

  
Signature

3-2-2000  
Date

00209071-030700

Applicants: ERIC HENDERSON and MICHAEL P. LYNCH  
Serial No.: To be Assigned  
Filed: March 7, 2000  
For: A METHOD FOR SOLID STATE GENOME ANALYSIS

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS  
(37 C.F.R. 1.9(f) and 1.27(c) - SMALL BUSINESS CONCERN)**

I hereby declare that I am

- ☐ the owner of the small business concern identified below:  
☒ an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: BioForce Laboratory, Inc.  
ADDRESS OF CONCERN: 2901 South Loop Drive, Ames, Iowa 50010

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 C.F.R. 121.3-18, and reproduced in 37 C.F.R. 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time, or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled A METHOD FOR SOLID STATE GENOME ANALYSIS by inventor(s) ERIC HENDERSON and MICHAEL P. LYNCH described in

- ☒ the specification filed herewith  
☐ application serial no. \_\_\_\_\_, filed \_\_\_\_\_  
☐ patent no. \_\_\_\_\_, issued \_\_\_\_\_

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below\* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 C.F.R. 1.9(d) or by any concern which would not qualify as a small business concern under 37 C.F.R. 1.9(d) or a nonprofit organization under 37 C.F.R. 1.9(e).

\*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities (37 C.F.R. 1.27).

FULL NAME: \_\_\_\_\_  
ADDRESS: \_\_\_\_\_  
☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

FULL NAME: \_\_\_\_\_  
ADDRESS: \_\_\_\_\_  
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I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 C.F.R. 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of Person Signing: ERIC HENDERSON  
Title of Person Other Than Owner: President  
Address of Person Signing: 2901 South Loop Drive, Ames, Iowa 50010

Signature Eric Henderson

Date: March 2, 2000

# **A Method for Solid State Genome Analysis**

## **TECHNICAL FIELD**

This application claims benefit from prior Provisional Application Serial No. 60/123,362, filed March 8, 1999.

5           This invention relates to the sequencing of DNA. More specifically, this invention is a method of mapping the relative positions of specific segments of nucleic acid using scanning probe microscopy.

## **BACKGROUND**

10           The human genome project is arguably the largest and most important scientific collaboration in history. Of more importance is the fact that the human genome project is just the beginning of the genome revolution. It is generally accepted that once the sequence of a genome is known, it can be “mined” for information that will be invaluable in deriving useful products such as new drugs, genetic medicines, improved animal and plant produce, and a host of others. While current methods are adequate for the human genome project to reach its projected completion date early in this millennium, there is ample room for improvements in technologies that would facilitate genome mapping efforts.

15           While a small number of important genomes are under analysis or have been fully sequenced, current methods are costly and limited in their speed. The genomes of a wide variety of health related and agriculturally relevant organisms remain to be explored. Using current methodology to repeat the effort spent on the human genome for every animal and plant that remains to be studied would be laborious and extremely time consuming. It is therefore essential that technological improvements in current genome analysis methods be invented and implemented to aid in this undertaking.

## Current Technology

The initial goal of all genome projects is to acquire the highest quality sequence data for the genome being studied. This is accomplished by determining the nucleotide sequence of fragments of the genome, and then assembling these sequence fragments into the complete genome sequence. There are no methods in existence for direct sequencing of an entire genome greater than a few thousand base pairs in a single experiment.

The current method for sequencing genomes involve first digesting the genomes with a restriction endonuclease. The genome is then subcloned into a variety of vectors including, but not limited to, plasmids, phage vectors, bacterial artificial chromosomes (BACs), and yeast artificial chromosomes (YACs). These fragments are still too large for direct sequencing, and must be further fragmented. The process of re-assembly of all the sequence information represented in these fragments is a formidable task. Current methods of genome analysis split the DNA (deoxyribonucleic acid) into many sub-genomic DNA fragments. These fragments are assembled into contiguous arrays known as “contigs.” There are two general prior art approaches to forming these contigs.

One prior art method used to form contigs is to identify nucleotide sequences by creating “restriction maps” of DNA fragments. These DNA fragments can serve to identify genomic fragments and also to identify the overlaps between fragments. A restriction map is a DNA profile that demarcates the positions of target sites for sequence specific restriction endonucleases along the length of the DNA. These maps are generated by digestion of the DNA with a restriction endonuclease and display of the digestion products by electrophoretic separation on a gel matrix, usually agarose or polyacrylamide. One advantage to this process is that it clearly defines which members of a large population or “library” of gene fragments still

need to be sequenced, thereby eliminating undesirable redundancy of effort. Furthermore, once each fragment has been mapped, the maps themselves can be used to determine the order of the fragments in the original sample. This process facilitates their sequential assembly into contigs. This process provides fragment size information, but must be repeated several times with a number of variations to allow deduction of the restriction fragment order in a large DNA sample. A need exists for a method that will reduce the effort, time and expense of the above method of nucleotide sequence mapping.

Other methods for characterizing genomic fragments also exist. For example, one common method known in the art as PCR footprinting uses defined sets of short oligonucleotide primers and generates a diagnostic set of PCR fragments from each genomic piece.

The second general prior art approach to genome analysis is to "shotgun" sequence randomly selected fragments and attempt to assemble them into the continuous genome sequence by locating sequence overlaps. This requires a large degree of redundancy in the sequencing effort. It is necessary to sequence many-fold more DNA than is contained in a single genome to insure that as many of the genes as possible have been included in the effort. While this approach works for small genomes, the requirement for redundancy of effort, coupled with the extremely low probability of obtaining sequence information for every gene in a genomic library, limit its utility. A need exists for a method that reduces the effort necessary to create these genomic libraries.

Both of these methods are facilitated by the use of physical markers to help identify the specific nucleotide sequence and produce a genomic map. The physical markers used can be produced in a variety of ways and with a wide range in precision. The markers can be genetic loci deduced from classical genetic approaches (e.g., genetic crosses and relative proximity



analysis) or more direct methods such as fluorescence *in situ* hybridization analysis (FISH). The former process is laborious and can be time consuming, especially in the case of slow growing organisms or organisms for which the genetic manipulation tools are rudimentary at best. The latter process requires that prior knowledge about the sequence of the genes under scrutiny be available.

It must be noted that for mapping a genome, it is necessary to have two libraries, each constructed using a different restriction endonuclease. This way, the fragments in the two libraries will overlap (since the two different restriction endonucleases cut the genome at different locations). Thus, by mapping the two libraries, and comparing the results, regions of overlap are discovered and this determines the physical order of the fragments in the genome. These fragments can then be sequenced and the entire genomic sequence determined.

### **Gene Fragment Polymorphisms (GFPs)**

In many cases it is of interest to compare DNA sequences from two sources. For example, in DNA “fingerprinting” applications one can use small variations in the sequence of DNA to determine the probability that a particular piece of DNA is derived from a given source. One method to do this is to compare the positions of target sites for endonucleases that cut DNA in a site specific fashion using a restriction endonuclease. If small changes have occurred in the defined DNA sequence from two sources, it is likely that the restriction endonuclease site map will reflect this, either by the gain or the loss of one or more sites. These changes are referred to as restriction fragment length polymorphisms, or RFLPs. RFLPs are a subset of all types of gene fragment polymorphisms, or GFPs. RFLP analysis is usually carried out by the conventional method described above, a restriction endonuclease digestion, followed by gel electrophoresis

and Southern blotting. A need exists for a method of analyzing these GFPs that would reduce the time and labor involved, as well as the expenditure on reagents required by these steps.

### **Functional Sequence Mapping**

A large portion of genomic DNA does not encode active genes. In addition, a significant portion of the functional component of a gene is never transcribed into RNA or used to construct a protein. However, these regulatory regions of genes are critical for expression of the gene product and play key roles as, for example, targets for new drugs that regulate levels of gene expression. To discover which regions are functional and which are not, with regard to gene activity, it is often necessary to do a large number of studies with large populations of sub fragments of the genome. This practice can take years of redundant, laborious, and expensive work.

### **Scanning Probe Microscopy and Atomic Force Microscopy**

A scanning probe microscope (SPM) utilizes a probe which is scanned over a surface. The interaction between the probe and surface is detected, recorded, and displayed. If the probe is small and kept very close to the surface, the resolution of the SPM can be very high, even on the atomic scale in some cases. There is a wide variety of SPM instruments capable of detecting optical, electronic, conductive, and other properties. One form of SPM, the atomic force microscope (AFM) is an ultra-sensitive force transduction system. In the AFM, a sharp tip is situated at the end of a flexible cantilever and scanned over a sample surface. While scanning, the cantilever is deflected by the net sum of the attractive and repulsive forces between the tip and sample. If the spring constant of the cantilever is known, the net interaction force can be accurately determined from the deflection of the cantilever. The deflection of the cantilever is usually measured by the reflection of a focused laser beam from the back of the cantilever onto a

split photodiode, constituting an “optical lever” or “beam deflection” mechanism. Other methods for the detection of cantilever deflection include interferometry and piezoelectric strain gauges. The first AFMs recorded only the vertical displacements of the cantilever. More recent methods involve resonating the tip and allowing only transient contact, or in some cases no contact at all, between it and the sample. Plots of tip displacement or resonance changes as it traverses a sample surface are used to generate topographic images. Such images have revealed the 3D structure of a wide variety of sample types including material, chemical and biological specimens. Some examples of the latter include DNA, proteins, chromatin, chromosomes, ion channels, and even living cells.

In addition to its imaging capabilities, the AFM can directly sense and measure forces in the microNewton ( $10^{-6}$ ) to picoNewton ( $10^{-12}$ ) range. Thus, the AFM can measure forces between molecular pairs, and even within single molecules. Moreover, the AFM can measure a wide variety of other forces and phenomena, such as magnetic fields, thermal gradients and viscoelasticity. This ability can be exploited to map force fields on a sample surface, and reveal with high resolution the location and magnitude of these fields, as in, for example, localizing magnetic microparticles tethered to biomolecular complexes of interest.

## **BRIEF DESCRIPTION OF THE DRAWINGS**

Figure 1 is a block diagram of the acts that comprise the method of the present invention.

## **SUMMARY**

One embodiment of the present invention relates to a method for determining the order of nucleic acid segments from a nucleic acid sample, the method comprising tagging sequence-specific sites of the nucleic acid sample with a sequence specific tag, scanning the nucleic acid

sample using a scanning probe microscope, and analyzing the scan of the nucleic acid sample to determine the order of nucleic acid segments.

A method for comparing DNA from two different sources, the method comprising tagging specific segments of a nucleic acid sample from a first source using a sequence specific tag, tagging specific segments of the nucleic acid sample from a second source using a sequence specific tag, scanning the tagged nucleic acid sample from the first source using a scanning probe microscope, scanning the tagged nucleic acid sample from the second source using a scanning probe microscope, analyzing the scan from the first source and the scan from the second source using a computer, and comparing the scan from the first source to the second source.

This embodiment analyzes DNA by way of example, but the present invention contemplates that any type of nucleic acid can be used as a sample in the sequencing method.

An object of this invention is use of SPM technology to identify defined sequence elements in nucleic acids fragments. The SPM scan further aids in the determination of the order of these elements on the nucleic acid of interest.

Another object of the present invention is to provide a method for simplifying DNA fingerprinting analysis.

A further object of the present invention is to provide a method for simplifying functional mapping of DNA fragments.

Yet another object of the present invention is a method for simplifying the mapping of DNA fragments such as BAC's and YAC's.

## DETAILED DESCRIPTION

The embodiment of the present invention disclosed herein is a method for analysis of populations of genomes and genomic fragments using a scanning probe microscope, such as an atomic force microscope or near field optical microscope. The physical maps created by this approach constitute genetic “bar codes” that can be used in a wide variety of gene identification and characterization applications. This method can be used to help the re-assembly of mapped DNA fragments back into the correct order. The AFM may also be used for rapid and precise mapping of target DNA samples such as cosmids, bacterial artificial chromosomes (BACs) and yeast artificial chromosomes (YACs). The invention described here also allows study of RFLPs, length polymorphisms generated by PCR methods, and other forms of GFPs (e.g., single point mutations). The AFM is used here by way of example, but this does not exclude use of other types of SPM instrumentation.

Figure 1 shows the acts that constitute the method of the present invention. In this embodiment a dipstick is used as the substrate onto which the functionalized DNA is bound for analysis. This dipstick facilitates the rapid mapping and analysis of sequence specific markers bound to large DNA molecules. However, the substrate to which the DNA is tethered is not exclusively in this form. The substrate for the tethering surface could be made of any compatible material known in the art and shaped in any form that can be scanned by the SPM instrumentation.

The DNA sample is first cut from the source and linearized (10). This material is then set aside while the dipstick surface is prepared (12). The dipstick surface is prepared by modifying it with a chemically reactive functional group so that the DNA can be tethered to the surface for eventual scanning by the SPM (14). The next step is modifying the DNA sample with the

appropriate functional group (16). This step will facilitate binding the DNA to the dipstick surface later in the method. Once the DNA is functionally modified, the DNA is then tethered to the dipstick surface (18). After the DNA is properly tethered, it is tagged with a sequence specific tag (20). The sequence specific tag is what is read (i.e., measured or detected) by the SPM. The tagged DNA is then dried (22) and aligned in a linear fashion on the dipstick surface. Drying ensures more stable imaging conditions and, therefore, optimizes data acquisition, although a drying step is not absolutely required. The tagged and tethered DNA on the dipstick is now scanned using the SPM instrument (24). In the last step, the readout from the SPM is analyzed (26).

Many of the steps of the present invention are not necessarily specific to the order as laid out in the following present embodiment. This embodiment is given by way of example. For instance, the surface can be prepared and modified after the DNA is functionalized instead of before.

### **Cutting/Linearization**

The first step of the method of the present invention involves obtaining the DNA sample to be analyzed (10). This is accomplished by cutting and linearizing the DNA to be analyzed. The DNA can be prepared by fragmenting the desired genomic DNA and ligating the fragments in a typical cloning vector known to those skilled in the art. The DNA can be excised from the source plasmid, cosmid, BAC, YAC or any nucleic acid vector using Bam H1 (*Bacillus amyloliquefaciens* H), EcoR1 (*E Coli restriction endonuclease number 1*), or any comparable restriction endonuclease, or other nuclease. DNA can also be prepared by mechanical methods such as shearing. The reaction conditions are determined by the choice of endonuclease and are common knowledge to those skilled in the art. The present embodiment utilizes a DNA sample

from a bacterial virus or phage, termed Lambda. This DNA sample is 48,502 base pairs long and constitutes the entire genome of the Lambda phage.

### **Surface Preparation**

The next act of the method is the selection of a surface (12). This surface will be the site where the DNA is deposited. The embodiment of the present invention utilizes a dipstick substrate to which to bind the DNA sample for scanning. In the present embodiment the dipstick is made of Teflon. Other plastics or inert polymers can be used in alternative embodiments. A small pad made of mica is attached to one end of the Teflon dipstick. Other embodiments may incorporate pads made of polished silicon or some similar material that is sufficiently flat to allow resolution of DNA fragments by AFM. Other surfaces include episilicon, highly ordered pyrolytic graphic, sapphire, gypsum, or coating with polystyrene and other defined surface coating materials. Any of these surfaces can also be coated with gold to facilitate formation of self assembled monolayers from alkanethiolate solutions. The advantage to this approach facilitates presentation of a wide variety of surface chemistries for various applications.

### **Surface Modification**

Once the dipstick surface is prepared, then the surface must be modified (14) so that it will react and tether the DNA for analysis. In the present embodiment the ability of alkanethiolates to form robust monolayers on gold surfaces is exploited. The gold is then coated with a chemically reactive alkanethiolate monolayer, the reactive portion in this example being either a carboxyl or succinimide group. These chemically active surfaces then serve as attachment points for the modified DNA.

In this embodiment a molecule containing a sulphydral group at one end, an 11 carbon alkane chain, and a succinimide group at the other end is used. This molecule is dissolved in

pure ethanol to a final concentration of 1mM. The gold coated surface is incubated in this solution for several hours at room temperature, allowing a stable monolayer to form. DNA that contains an amino group modification at the terminus can then be immobilized on this surface by formation of an amide bond between the succinimide group on the alkane and the primary amine on the DNA.

An advantage of this method is that it can be used to create hydrophilic domains surrounded by hydrophobic domains to which the DNA will not have a high affinity in solution. This facilitates “floating” the DNA away from the surface during the tagging procedure to minimize stereochemical hindrance, then deposition of the DNA on the surface by virtue of dehumidification, which abrogates the hydrophobic effect. To create these surfaces, the first step is to produce a uniform monolayer of methyl-terminated (hydrophobic) alkanethiolates on a gold surface. The gold surface can be modified with a pattern such as stripes or checkerboard arrays by evaporation of gold through a mask in order to create different areas to which to bind the DNA. UV light is then passed through a mask to oxidize the sulfur atom on the alkanethiolate. This treatment weakens the sulfur/gold interaction considerably, but only in the those regions subjected to the UV irradiation. Subsequent addition of a succinimide terminated alkanethiolate results in replacement of the oxidized thiolates with the succinimide terminated molecules and creation of a patterned array of chemically active domains to which DNA can be specifically tethered. Variations of this method are known to those skilled in the art.

Alternative methods for surface modification include preparing a positively charged surface by modification of the surface using a silane compound containing primary amines. Another embodiment includes spin coating a mica or polished silicon surface with a preparation of polystyrene. The polystyrene is prepared by dissolution in toluene. Each one of these



alternative methods for surface modification will have a resulting alternative embodiment for the DNA modification of the next step. A functional group must be placed on the DNA that will correspondingly react with the surface to tether the DNA. The present invention contemplates utilizing any of these alternative methods.

## **DNA Modification**

Linearized DNA is modified at one or both ends with a reactive group that allows the DNA molecule to be firmly tethered to a surface (16). In this embodiment, the DNA is modified with a primary amine group to allow covalent bonding to the surface bound succinimide group. The linearized DNA contains staggered or "sticky" ends by virtue of its release from the cloning vector by a restriction endonuclease, or, in the case described above (Lambda DNA) the natural ends of the Lambda genome are staggered (note that fragments cleaved from cosmids at the COS site will have the same 12 nucleotide sticky end as Lambda phage). Since this sequence is known, a complementary molecule containing the amino terminal group is synthesized by standard methods known to those skilled in the art. This material can alternatively be purchased from a commercial vendor of synthetic DNA oligonucleotides. The amino terminated oligonucleotide is ligated to the linearized DNA fragment using T4 DNA ligase and standard conditions known to those skilled in the art. The ligation product is then rapidly purified chromatographically and tethered to the surface as described below. Other methods known to those skilled in the art can likewise be used to separate large and small DNA fragments.

## **DNA Deposition and Tethering DNA to the Surface**

Although the details of DNA deposition vary, the present embodiment contemplates depositing a small droplet of DNA solution on a surface and allowing the DNA to bind to the surface through an end-specific tether (18).



## Sequence Specific Tagging of Immobilized DNA

In the next step the DNA is tagged with a sequence specific tag (20). In the present embodiment the DNA is incubated with a mutated restriction endonuclease in a typical restriction endonuclease reaction solution (25 mM buffer, pH 7.6; 100 mM monovalent cation, typically  $\text{Na}^+$ , 10 mM divalent cation, typically  $\text{Mg}^{++}$ , 0.5 mM reducing agent, typically dithiothreitol). The mutant restriction endonuclease has been modified by amino acid substitution within its catalytic pocket such that the endonuclease can bind its DNA target site, but is incapable of cutting the DNA. This substitution promotes DNA binding but inhibits cleavage. (see D. Allison, P. Kerper, M. Doktycz, J. Spain, P. Modrich, F. Larimer, T. Thundat, and R. Warmack, Proc. Natl. Acad. Sci. USA, 1996. 93: p. 8826-8829). This is accomplished by genetic engineering methods known to practitioners skilled in the art.

Wild type restriction enzymes can also be used by substituting  $\text{Ca}^{++}$  or  $\text{Mn}^{++}$  for  $\text{Mg}^{++}$ , the common catalytic divalent cation. In the presence of  $\text{Ca}^{++}$  or  $\text{Mn}^{++}$ , but the absence of  $\text{Mg}^{++}$ , many restriction endonucleases will bind but not cleave DNA. This is because  $\text{Mg}^{++}$  is required for catalytic activity of the endonuclease. The conditions for binding but not cutting of the DNA for each restriction endonuclease used are optimized using electrophoretic mobility shift experiments, a method whose application for this purpose is common knowledge to those skilled in the art.

The restriction endonuclease tag binds to the DNA, and the surface is quickly rinsed to remove spuriously bound tag molecules and other debris, such as excess salt. In some cases the tag can be fixed in position using UV light or a crosslinker such as glutaraldehyde. Other endonucleases can be used that have been modified such that they bind tightly to DNA but do not cut the DNA molecule. Those endonucleases that bind tightly to a defined nucleotide sequence,



## Scanning

Scanning of the tagged nucleic acid sample in the present embodiment is done utilizing an atomic force microscope (24). The sample is placed in the instrument. A Digital Instruments, Inc., Dimension 3100 is used in this embodiment and is controlled by a computer and software generally available. The computer controls the operation of the tip across the dipstick. In the present embodiment the nucleic acid samples have been tethered to specific sites on the stick. The computer can automatically scan these sections and report where the tags are found, and measure both the contour locations of the tags as well as the distance between the contours. Knowing where the DNA is specifically bound to the surface aids the analysis of the scan. Since the conventional AFM is limited in scan field size to about 100 square microns, knowing where the DNA array is located and the positions of the DNA molecules within the array greatly speeds the scanning process. Therefore, each array of DNA molecules is initially located through the use of a physical mark such as an indentation or ink spot, then the array is scanned and the positions of the molecules within the array noted.

The analysis conditions of this embodiment require low humidity because it minimizes potentially destructive tip-sample capillary forces and provides a more stable DNA specimen. The instrument takes data scans of the different sequence specific tags it has located and then feeds this data to the user who can analyze the output. In other embodiments low humidity might not be desirable, i.e. using the above method and scanning the sample while in solution.

Because in the present embodiment the DNA is displayed in an ordered array on solid state surfaces, the array can be processed continuously in the SPM. Through the use of indexing markers on the surface of the dipstick, the instrumentation can know precisely the position of the current scan, and therefore the sample that is currently being processed. A bar code is assigned

to the known sample, making that DNA fragment uniquely identifiable thereafter by virtue of its bar code.

### Analyzing the Scan

Software known by those skilled in the art runs the scan by the AFM (26). This software  
5 utilizes pattern recognition algorithms that direct the instrumentation to produce a hardcopy output.

In the present embodiment, the AFM data is collected using commercial software supplied with the instrument. This data is then ported to a separate computer using a software program called IDEAS (NanoStar, Baltimore, MD). IDEAS searches the field and finds  
10 continuous data profiles that correspond to intact, linear DNA molecules. IDEAS then measures the contour length of the molecules and locates the physical markers comprised of bound EcoR1 molecules. The software then plots these locations as a function of fragment length and generates a histogram showing the probability of finding a physical marker at a given position along the length of the DNA molecule. These data are averaged and used to generate a  
15 diagnostic bar code for that particular DNA molecule. By measuring the distance between the tags, the length of the DNA fragment between the tags can be ascertained. The order in which the segments appear on the contig, can be learned utilizing data from several different tagged nucleic acid samples.

The bar codes represent the nucleic acid fragment. Each bar of the code is where the  
20 AFM has found one of the sequence specific tags. The distances between the bars is the distance between the located tags. By aligning the bars from separate bar codes, the order of each known fragment can be determined.

The scan can be analyzed by several other methods known in the art. The most basic method of analyzing the scan is to measure by hand the contours that have been given as output from the SPM instrument.

The alternative embodiments could utilize a computer program which could analyze the information on the location of the sequence specific tags and the distance between them. This computer then would use an algorithm to place the fragments in the proper order as they appear on the original nucleic acid sample.

An advantage to the present invention is the bar code system of analyzing the scans. Utilizing a bar code enables faster ordering of the fragments. Before, researchers had to map the sequence of the fragment in order to determine the order of the fragments in the sample. The present invention allows the user to utilize the bar code of each fragment to align the overlapping fragments in the order they appear on the cosmid without having to determine the sequence of large sections of the sample.

#### **Further Embodiments and Advantages**

An alternative embodiment could be to apply this method to comparing DNA sequences from two sources. To do this, a sequence specific tag would be utilized that would bind onto an area where it is thought a nucleotide sequence variation might occur. Once the sequence specific tags were placed on the DNA fragments utilizing the method described above, the fragments would be scanned in the SPM. If a tag appears on a section of the DNA in both the samples then it would increase the likelihood that the samples came from the same source. By choosing the sequence specific tag that binds on to an unusual nucleotide sequence, accurate fingerprinting can be done without the long process of restriction fragment length polymorphisms utilizing gel electrophoresis and Southern blotting.

A further embodiment of the present invention involves functional sequence mapping.

As discussed above, a large portion of genomic DNA does not encode active genes. Using the above method this invention allows rapid analysis of genomes using markers that specifically tag regions involved in gene activity. Once the DNA is tagged with these sequence specific markers, the DNA fragment can be analyzed by the SPM. The location of the sequence specific tags will report where the active encoding regions are located on the original DNA fragment.

A further embodiment of the present invention involves identification of single nucleotide polymorphisms. It has been suggested that individual humans have a single nucleotide variation relative to any other individual every 900 basepairs. These variations can be valuable markers associated with genetic traits such as predisposition to disease. The maps generated by the method described here can reveal single nucleotide polymorphisms because such a change in sequence can preclude or allow binding of the tag to a particular sequence element.

The information and examples described herein are for illustrative purposes and are not meant to exclude any derivations or alternative methods that are within the conceptual context of the invention. It is contemplated that various deviations can be made to this embodiment without deviating from the scope of the present invention. Accordingly, it is intended that the scope of the present invention be dictated by the appended claims rather than by the foregoing description of this embodiment.



## Claims

1. A method for analyzing a nucleic acid sample, the method comprising:
  - (a) tagging sequence specific sites of the nucleic acid sample;
  - (b) scanning the nucleic acid sample; and
  - (c) analyzing the scan of the nucleic acid sample.
2. The method of claim 1 wherein said tagging step further comprises tagging with a sequence specific tag.
3. The method of claim 1 wherein said scanning step comprises utilizing a scanning probe microscope.
4. The method of claim 1 wherein said scanning step comprises utilizing an atomic force microscope.
5. The method of claim 1 wherein said scanning step the comprises utilizing a near field optical microscope.
6. The method of claim 1 wherein said analyzing step comprises analyzing the scan using a computer.
7. The method of claim 1 wherein said sequence-specific tag is chosen from one or more of the group comprising of a restriction endonuclease, a transcription factor, a modified nucleotide, a peptide, a nucleotide, and a small molecule conjugated to a microparticle or a nanoparticle.

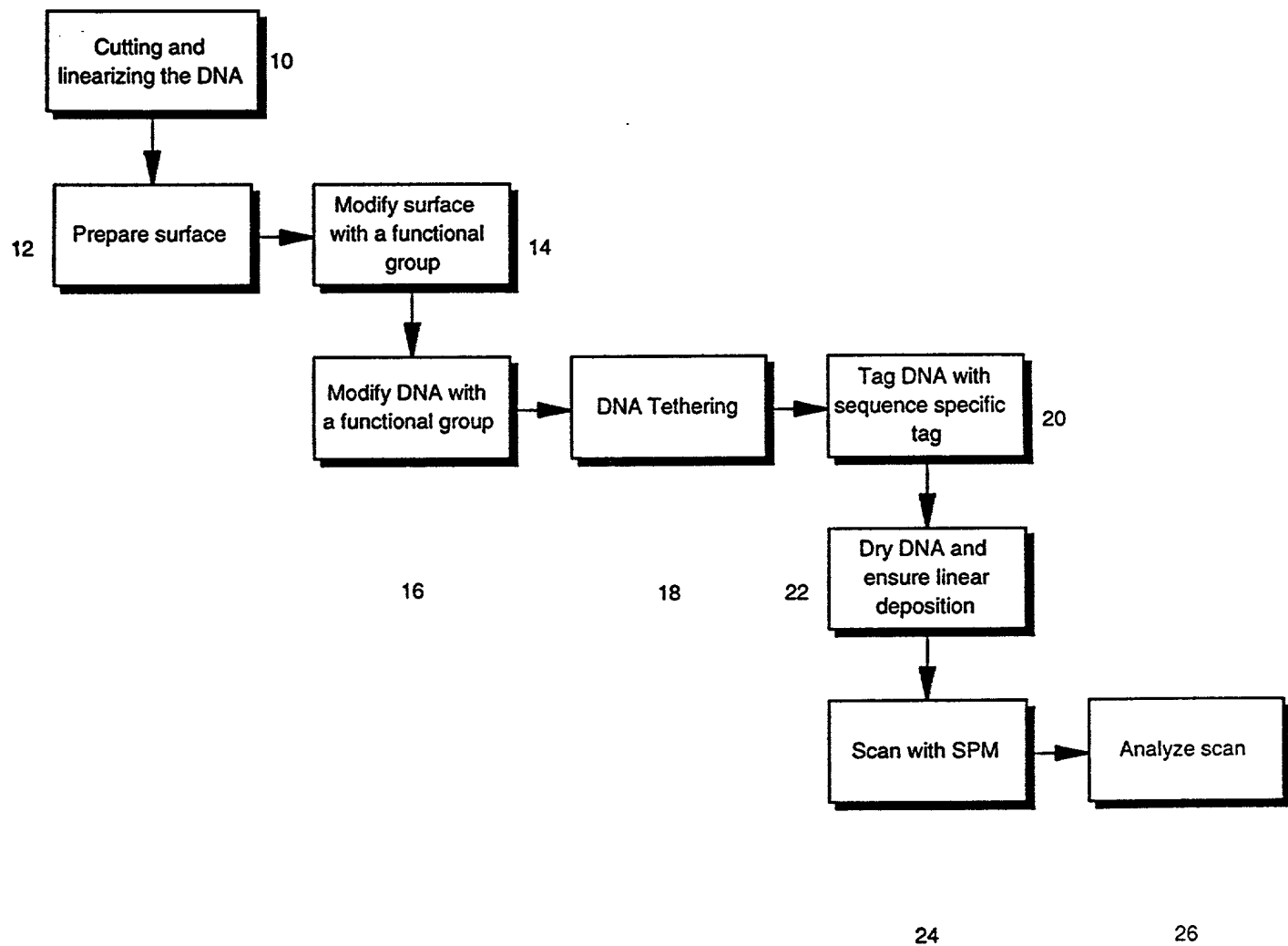
8. The method of claim 1 wherein the sequence-specific tag is a duplex, a triplex, or a quadruplex performing legate.
9. The method of claim 1 wherein the nucleic acid sample is DNA chosen from one or more of the group comprising a cosmid, a bacterial artificial chromosome, or a yeast artificial chromosome.
10. The method of claim 1 wherein said analyzing step further comprises creating a bar code and comparing the bar codes from different samples.
11. The method of claim 1 further comprising linearizing the nucleic acid sample.
12. The method of claim 1 further comprising cutting the nucleic acid sample with a restriction endonuclease.
13. The method of claim 12, further comprising
- (a) modifying the cut nucleic acid sample with a functional group; and
  - (b) tethering the nucleic acid sample to a deposition surface.
14. The method of claim 13 further comprising drying the deposition surface to which the modified nucleic acid is tethered.
15. The method of claim 14 further comprising ensuring the tethered nucleic acid sample is linearly deposited on the deposition surface.
16. The method of claim 15 wherein the functional group is chosen from the group one or more of the group comprising biotin-avidin complexes, primary amines, sulfhydryl groups, single stranded binding proteins, or histidine terminated oligonucleotides.
17. The method of claim 16 wherein the deposition surface is located on a dipstick.

18. The method of claim 17 wherein the deposition surface of the dipstick has specific areas for tethering different types of functional group modified nucleic sequences.
19. A method for locating the functional segments of a nucleic acid sample, the method comprising
- (c) tagging sites of the nucleic acid sample;
- (d) scanning the nucleic acid sample using a scanning probe microscope;
- (e) analyzing the scan of the nucleic acid sample to determine the location of the functional segments of the nucleic acid sample.
20. The method of claim 19 wherein the functional segment of the nucleic acid sample is chosen from one or more of the group comprising a promoter, an enhancer, an attenuator, and a silencer.
21. The method of claim 20 further comprising linearizing the nucleic acid sample.
22. The method of claim 21 further comprising cutting the nucleic acid sample with a restriction endonuclease.
23. The method of claim 22, further comprising
- (f) modifying the cut nucleic acid sample with a functional group; and
- (g) tethering the modified nucleic acid sample to a deposition surface.
24. The method of claim 23 further comprising drying the deposition surface to which the modified nucleic acid sample is tethered.
25. The method of claim 24 further comprising ensuring the tethered nucleic acid sample is linearly deposited on the deposition surface.

26. The method of claim 25 wherein the functional group is chosen from one or more of the group comprising biotin-avidin complexes, primary amines, sulfhydryl groups, single stranded binding proteins, or histidine terminated oligonucleotides.
27. The method of claim 26 wherein the deposition surface is located on a dipstick.
28. The method of claim 27 wherein the deposition surface of the dipstick has a specific areas for tethering different types of functional group modified nucleic acid sample.
29. A method for comparing DNA from two different sources, comprising:
- (h) tagging a nucleic acid sample from a first source;
  - (i) tagging a nucleic acid sample from a second source;
  - (j) scanning the tagged nucleic acid sample from the first source;
  - (k) scanning the tagged nucleic acid sample from the second source;
  - (l) analyzing the scan from the first source and the scan from a second source using a computer; and
  - (m) comparing the scan from the first source to the scan from the second source.
30. The method of claim 29 wherein said scanning further comprises utilizing a scanning probe microscope.
31. The method of claim 29 wherein the comparison allows the detection of single nucleotide polymorphisms between the DNA sources.

## Abstract

The invention is a solid state process for analyzing genomes by visualizing sequence specific markers (e.g., proteins that bind defined DNA sequence elements) by scanning probe microscopy. The method includes linear display of the nucleic acid on a solid surface, image acquisition by the scanning probe microscope, and digital data analysis. The acts of the method result in a bar code type display of each fragment of the DNA sample. These bar codes are then used to place the fragments in the order they appear on the original DNA sample.



## **DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled A METHOD FOR SOLID STATE GENOME ANALYSIS, the specification of which

- ☒ is attached hereto.
- ☐ was filed on \_\_\_\_\_ as United States application number \_\_\_\_\_ and amendment on \_\_\_\_\_.

I do not know and do not believe that the invention was ever known or used in the United States before my or our invention thereof;

I do not know and do not believe that the invention was ever patented or described in any printed publication in any country before my or our invention thereof or more than one year prior to this application;

I do not know and do not believe that the invention was in public use or on sale in the United States more than one year prior to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT international application which designated at least one country other than the United States, listed below, and I have also identified and listed below any foreign application(s) for patent or inventor's certificate, or PCT international application, having a filing date before that of the application(s) on which priority is claimed:

### FOREIGN APPLICATION(S)

Number	Country	day/month/year filed	Priority Claimed

I hereby claim the benefit under Title 35, United States Code, Section 119(e) of any U.S. provisional application(s) listed below:

### U.S. PROVISIONAL APPLICATION(S)

Application Serial No.	Filing Date
60/123,362	March 8, 1999

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s), or under Section 365(c) of any PCT international application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

### PRIORITY U.S. APPLICATION(S)

Application Serial No.	Filing Date	Status

### POWER OF ATTORNEY

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: Brian J. Laurenzo (Registration No. 34,207) and Michael C. Gilchrist (Registration No. 40,619).

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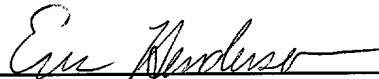
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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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